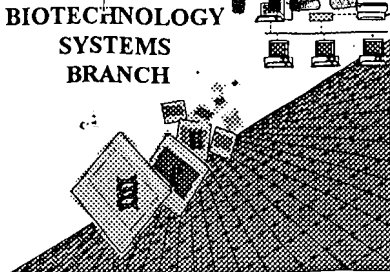


RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

FILE COPY



HA/
DB
4/6/01

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer-readable form:

Application Serial Number: 09/267,963B

Source: 1647

Date Processed by STIC: 3/27/2001

RECEIVED

APR 04 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/267963B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☒ **Misaligned Amino Acid Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ **PatentIn ver. 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ **Skipped Sequences (OLD RULES)** Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ **Skipped Sequences (NEW RULES)** Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ **Use of <213>Organism (NEW RULES)** Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ **Use of <220>Feature (NEW RULES)** Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ **PatentIn ver. 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted "file," resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/267,963BDATE: 04/02/2001
TIME: 22:24:55

INPUT SET: S36584.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

pr 2, 4-5

SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

(1) General Information:

(i) APPLICANT: Kohei MIYAZONO; Takeshe IMAMURA; Peter DEN DIJKE

(ii) TITLE OF INVENTION: ISOLATED ALK-1 PROTEIN, NUCLEIC ACIDS ENCODING
IT, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 46

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fulbright & Jaworski L.L.P.
(B) STREET: 666 Fifth Avenue
(C) CITY: New York City
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10103

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/267,963
(B) FILING DATE: March 12, 1999
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/GB93/02367
(B) FILING DATE: November 17, 1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9224057.1
(B) FILING DATE: November 17, 1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9304677.9
(B) FILING DATE: March 8, 1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9304680.3
(B) FILING DATE: March 8, 1993

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/267,963BDATE: 04/02/2001
TIME: 22:24:55

INPUT SET: S36584.raw

46
47 (vii) PRIOR APPLICATION DATA:
48 (A) APPLICATION NUMBER: 9311047.6
49 (B) FILING DATE: May 28, 1993
50
51 (vii) PRIOR APPLICATION DATA:
52 (A) APPLICATION NUMBER: 9313763.6
53 (B) FILING DATE: July 2, 1993
54
55 (vii) PRIOR APPLICATION DATA:
56 (A) APPLICATION NUMBER: 9136099.2
57 (B) FILING DATE: August 3, 1993
58
59 (vii) PRIOR APPLICATION DATA:
60 (A) APPLICATION NUMBER: 321344.5
61 (B) FILING DATE: October 15, 1993
62
63 (vii) PRIOR APPLICATION DATA:
64 (A) APPLICATION NUMBER: 09/039,177
65 (B) FILING DATE: March 13, 1998
66
67 (viii) ATTORNEY/AGENT INFORMATION:
68 (A) NAME: Mary Anne Schofield
69 (B) REGISTRATION NUMBER: 36,669
70 (C) REFERENCE/DOCKET NUMBER: LUD 5539.1 CIP - JEL/MAS
71
72 (ix) TELECOMMUNICATION INFORMATION:
73 (A) TELEPHONE: (212) 318-3000
74 (B) TELEFAX: (212) 318-3400
75
76

ERRORED SEQUENCES FOLLOW:

2716 (2) INFORMATION FOR SEQ ID NO: 34:
2717 (i) SEQUENCE CHARACTERISTICS:
2718 (A) LENGTH: 513 amino acids
--> 2719 (B) ~~TYPE: amino acid~~ → delete "7"
2720 (D) TOPOLOGY: linear
2721
2722 (ii) MOLECULE TYPE: peptide
2723
2724 (vi) ORIGINAL SOURCE:
2725 (A) ORGANISM: MOUSE
2726
2727 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
2728
2729 Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
2730 5 10 15
2731 Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe

RAW SEQUENCE LISTING PATENT APPLICATION US/09/267,963B

DATE: 04/02/2001
TIME: 22:24:55

INPUT SET: S36584.raw

2732		20		25		30											
2733	Phe	Asn	Ala	Asn	Trp	Glu	lys	Asp	Arg	Thr	Asn	Gln	Thr	Gly	Val	Glu	
2734			35					40					45				
2735	Pro	Cys	Tyr	Gly	Asp	Lys	Asp	Lys	Arg	Arg	His	Cys	Phe	Ala	Thr	Trp	
2736			50					55					60				
2737	Lys	Asn	Ile	Ser	Gly	Ser	Ile	Glu	Ile	Val	Lys	Gln	Gly	Cys	Trp	Leu	
2738			65					70					75			80	
2739	Asp	Asp	Ile	Asn	Cys	Tyr	Asp	Arg	Thr	Asp	Cys	Val	Glu	Lys	Lys	Asp	
2740					85					90					95		
2741	Ser	Pro	Glu	Val	Tyr	Phe	Cys	Cys	Cys	Glu	Gly	Asn	Met	Cys	Asn	Glu	
2742				100						105				110			
2743	Lys	Phe	Ser	Tyr	Phe	Pro	Glu	Met	Glu	Val	Thr	Gln	Pro	Thr	Ser	Asn	
2744				115						120				125			
2745	Pro	Val	Thr	Pro	Lys	Pro	Pro	Tyr	Tyr	Asn	Ile	Leu	Leu	Tyr	Ser	Leu	
2746				130						135				140			
2747	Val	Pro	Leu	Met	Leu	Ile	Ala	Gly	Ile	Val	Ile	Cys	Ala	Phe	Trp	Val	
2748						150					155					160	
2749	Tyr	Arg	His	His	Lys	Met	Ala	Tyr	Pro	Pro	Val	Leu	Val	Pro	Thr	Gln	
2750					165					170					175		
2751	Asp	Pro	Gly	Pro	Pro	Pro	Pro	Ser	Pro	Leu	Leu	Gly	Leu	Lys	Pro	Leu	
2752				180						185				190			
2753	Gln	Leu	Leu	Glu	Val	Lys	Ala	Arg	Gly	Arg	Phe	Gly	Cys	Val	Trp	Lys	
2754				195				200					205				
2755	Ala	Gln	Leu	Leu	Asn	Glu	Tyr	Val	Ala	Val	Lys	Ile	Phe	Pro	Ile	Gln	
2756				210				215					220				
2757	Asp	Lys	Gln	Ser	Trp	Gln	Asn	Glu	Tyr	Glu	Val	Tyr	Ser	Leu	Pro	Gly	
2758						230					235					240	
2759	Met	Lys	His	Glu	Asn	Ile	Leu	Gln	Phe	Ile	Gly	Ala	Glu	Lys	Arg	Gly	
2760					245					250					255		
2761	Thr	Ser	Val	Asp	Val	Asp	Leu	Trp	Leu	Ile	Thr	Ala	Phe	His	Glu	Lys	
2762				260						265				270			
2763																	
2764	Gly	Ser	Leu	Ser	Asp	Phe	Leu	Lys	Ala	Asn	Val	Val	Ser	Trp	Asn	Glu	
2765				275				280					285				
2766	Leu	Cys	His	Ile	Ala	Glu	Thr	Met	Ala	Arg	Gly	Leu	Ala	Tyr	Leu	His	
2767				290				295					300				
2768	Glu	Asp	Ile	Pro	Gly	Leu	Lys	Asp	Gly	His	Lys	Pro	Ala	Ile	Ser	His	
2769						310					315					320	
2770	Arg	Asp	Ile	Lys	Ser	Lys	Asn	Val	Leu	Leu	Lys	Asn	Asn	Leu	Thr	Ala	
2771					325					330					335		
2772	Cys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Leu	Lys	Phe	Glu	Ala	Gly	Lys	Ser	
2773				340					345					350			
2774	Ala	Gly	Asp	Thr	His	Gly	Gln	Val	Gly	Thr	Arg	Arg	Tyr	Met	Ala	Pro	
2775				355				360					365				
2776	Glu	Val	Leu	Glu	Gly	Ala	Ile	Asn	Phe	Gln	Arg	Asp	Ala	Phe	Leu	Arg	
2777				370				375					380				
2778	Ile	Asp	Met	Tyr	Ala	Met	Gly	Leu	Val	Leu	Trp	Glu	Leu	Ala	Ser	Arg	
2779						390					395					400	
2780	Cys	Thr	Ala	Ala	Asp	Gly	Pro	Val	Asp	Glu	Tyr	Met	Leu	Pro	Phe	Glu	
2781					405					410					415		
2782	Glu	Glu	Ile	Gly	Gln	His	Pro	Ser	Leu	Glu	Asp	Met	Gln	Glu	Val	Val	
2783				420					425					430			
2784	Val	His	Lys	Lys	Lys	Arg	Pro	Val	Leu	Arg	Asp	Tyr	Trp	Gln	Lys	His	

RAW SEQUENCE LISTING PATENT APPLICATION US/09/267,963B

DATE: 04/02/2001
TIME: 22:24:56

INPUT SET: S36584.raw

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2785      435      440      445
2786 Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His
2787      450      455      460
2788 Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
2789      465      470      475      480
2790 Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
2791      485      490      495
2792 Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser
2793      500      505      510
2794 Leu
2795
2796

```

2967 (2) INFORMATION FOR SEQ ID NO: 37:

2968 (i) SEQUENCE CHARACTERISTICS:

--> 2969 (A) LENGTH: 102 amino acids → 99 shown

--> 2970 (B) TYPE: amino acid → delete ?

2971 (D) TOPOLOGY: linear

2972 (ii) MOLECULE TYPE: peptide

2973 (vi) ORIGINAL SOURCE:

2974 (A) ORGANISM: C. elegans

2975 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

2976 Cys His Cys Ser Arg Glu Val Gly Cys Asn Ala Arg Thr Thr Gly Trp

2977 Val Pro Gly Ile Glu Phe Leu Asn Glu Thr Asp Arg Ser Phe Tyr Glu

2978 Asn Thr Cys Tyr Thr Asp Gly Ser Cys Tyr Gln Ser Ala Arg Pro Ser

2979 Pro Glu Ile Ser His Phe Gly Cys Met Asp Glu Lys Ser Val Thr Asp

2980 Glu Thr Glu Phe His Asp Thr Ala Ala Lys Val Cys Thr Asn Asn Thr

2981 Lys Asp Pro His Ala Thr Val Trp Ile Cys Cys Asp Lys Gly Asn Phe

2982 Cys

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/267,963B

DATE: 04/02/2001
TIME: 22:24:56

INPUT SET: S36584.raw

3129 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

3130

3131 Gly Thr Ala Arg Tyr Met

3132

3133

5S
misaligned number

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/267,963BDATE: 04/02/2001
TIME: 22:24:56*INPUT SET: S36584.raw*

Line	Error	Original Text
29	Wrong Classification	(C) CLASSIFICATION: 435
2719	Unknown or Misplaced Identifier	(B) TY7PE: amino acid
2969	Entered (102) and Calc. Seq. Length (97) differ	(A) LENGTH: 102 amino acids
2970	Unknown or Misplaced Identifier	(B) TY7PE: amino acid
3123	Length must be an Integer	(A) LENGTH: amino acids
3123	Entered (0) and Calc. Seq. Length (6) differ	(A) LENGTH: amino acids